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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/687,230  
DATE: 10/27/2000  
TIME: 13:14:26

Input Set : A:\1027-seq.app  
Output Set: N:\CRF3\10272000\I687230.raw

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3 <110> APPLICANT: Braselmann, Sylvia
5 <120> TITLE OF INVENTION: Nucleotide Sequences that Encode
6   Phosphatidylinositol-3' Kinase Associated Proteins and
7   Uses Thereof
9 <130> FILE REFERENCE: 1027-DIV1
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/687,230
12 <141> CURRENT FILING DATE: 2000-10-13
14 <150> PRIOR APPLICATION NUMBER: 08/942,008
15 <151> PRIOR FILING DATE: 1997-10-01
17 <150> PRIOR APPLICATION NUMBER: 60/030,103
18 <151> PRIOR FILING DATE: 1996-11-01
20 <160> NUMBER OF SEQ ID NOS: 2
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2307
26 <212> TYPE: DNA
27 <213> ORGANISM: PI3' Kinase
29 <220> FEATURE:
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33 <400> SEQUENCE: 1
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36 gcgggccccg ctcccgccct ccgctcgccct ggcccgacc ggaagcggcg ccgcacggcc 120
38 tgggcctggc gcggggggcg ggcaccgggg ccggtcgga c atg ggc aag aag cac 176
W--> 39                                     Met Gly Lys Lys His
40                                     1           5
42 aag aag cac aag tcg gac aaa cac ctc tac gag gag tat gta gag aag 224
43 Lys Lys His Lys Ser Asp Lys His Leu Tyr Glu Glu Tyr Val Glu Lys
44           10           15           20
46 ccc ttg aag ctg gtc ctc aaa gta gga ggg aac gaa gtc acc gaa ctc 272
47 Pro Leu Lys Leu Val Leu Lys Val Gly Gly Asn Glu Val Thr Glu Leu
48           25           30           35
50 tcc acg ggc agc tcg ggg cac gac tcc agc ctc ttc gaa gac aaa aac 320
51 Ser Thr Gly Ser Ser Gly His Asp Ser Ser Leu Phe Glu Asp Lys Asn
52           40           45           50
54 gat cat gac aaa cac aag gac aga aag cgg aaa aag aga aag aaa gga 368
55 Asp His Asp Lys His Lys Asp Arg Lys Arg Lys Lys Arg Lys Lys Gly
56           55           60           65
58 gag aag cag att cca ggg gaa gaa aag ggg aga aaa cgg aga aga gtt 416
59 Glu Lys Gln Ile Pro Gly Glu Glu Lys Gly Arg Lys Arg Arg Arg Val
60           70           75           80           85
62 aag gag gat aaa aag aag cga gat cga gac cgg gtg gag aat gag gca 464
63 Lys Glu Asp Lys Lys Lys Arg Asp Arg Asp Arg Val Glu Asn Glu Ala
64           90           95           100
66 gaa aaa gat ctc cag tgt cac gcc cct gtg aga tta gac ttg cct cct 512
67 Glu Lys Asp Leu Gln Cys His Ala Pro Val Arg Leu Asp Leu Pro Pro
68           105           110           115

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70 gag aag cct ctc aca agc tct tta gcc aaa caa gaa gaa gta gaa cag 560
71 Glu Lys Pro Leu Thr Ser Ser Leu Ala Lys Gln Glu Glu Val Glu Gln
72      120      125      130
74 aca ccc ctt caa gaa gct ttg aat caa ctg atg aga caa ttg cag aga 608
75 Thr Pro Leu Gln Glu Ala Leu Asn Gln Leu Met Arg Gln Leu Gln Arg
76      135      140      145
78 aaa gat cca agt gct ttc ttt tca ttt cct gtg act gat ttt att gct 656
79 Lys Asp Pro Ser Ala Phe Ser Phe Pro Val Thr Asp Phe Ile Ala
80 150      155      160      165
82 cct ggc tac tcc atg atc att aaa cac cca atg gat ttt agt acc atg 704
83 Pro Gly Tyr Ser Met Ile Ile Lys His Pro Met Asp Phe Ser Thr Met
84      170      175      180
86 aaa gaa aag atc aag aac aat gac tat cag tcc ata gaa gaa cta aag 752
87 Lys Glu Lys Ile Lys Asn Asn Asp Tyr Gln Ser Ile Glu Glu Leu Lys
88      185      190      195
90 gat aac ttc aaa cta atg tgt act aat gcc atg att tac aat aaa cca 800
91 Asp Asn Phe Lys Leu Met Cys Thr Asn Ala Met Ile Tyr Asn Lys Pro
92      200      205      210
94 gag acc att tat tat aaa gct gca aag aag ctg ttg cac tca gga atg 848
95 Glu Thr Ile Tyr Tyr Lys Ala Ala Lys Lys Leu Leu His Ser Gly Met
96      215      220      225
98 aaa att ctt agc cag gaa aga att cag agc ctg aag cag agc ata gac 896
99 Lys Ile Leu Ser Gln Glu Arg Ile Gln Ser Leu Lys Gln Ser Ile Asp
100 230      235      240      245
102 ttc atg gct gac ttg cag aaa act cga aag cag aaa gat gga aca gac 944
103 Phe Met Ala Asp Leu Gln Lys Thr Arg Lys Gln Lys Asp Gly Thr Asp
104      250      255      260
106 acc tca cag agt ggg gag gac gga ggc tgc tgg cag aga gag aga gag 992
107 Thr Ser Gln Ser Gly Glu Asp Gly Gly Cys Trp Gln Arg Glu Arg Glu
108      265      270      275
110 gac tct gga gat gcc gaa gca cac gcc ttc aag agt ccc agc aaa gaa 1040
111 Asp Ser Gly Asp Ala Glu Ala His Ala Phe Lys Ser Pro Ser Lys Glu
112      280      285      290
114 aat aaa aag aaa gac aaa gat atg ctt gaa gat aag ttt aaa agc aat 1088
115 Asn Lys Lys Lys Asp Lys Asp Met Leu Glu Asp Lys Phe Lys Ser Asn
116      295      300      305
118 aat tta gag aga gag cag gag cag ctt gac cgc atc gtg aag gaa tct 1136
119 Asn Leu Glu Arg Glu Gln Glu Gln Leu Asp Arg Ile Val Lys Glu Ser
120 310      315      320      325
122 gga gga aag ctg acc agg cgg ctt gtg aac agt cag tgc gaa ttt gaa 1184
123 Gly Gly Lys Leu Thr Arg Arg Leu Val Asn Ser Gln Cys Glu Phe Glu
124      330      335      340
126 aga aga aaa cca gat gga aca acg acg ttg gga ctt ctc cat cct gtg 1232
127 Arg Arg Lys Pro Asp Gly Thr Thr Thr Leu Gly Leu Leu His Pro Val
128      345      350      355
130 gat ccc att gta gga gag cca ggc tac tgc ctg gtg aga ctg gga atg 1280
131 Asp Pro Ile Val Gly Glu Pro Gly Tyr Cys Leu Val Arg Leu Gly Met
132      360      365      370
134 aca act gga aga ctt cag tct gga gtg aat act ttg cag ggg ttc aaa 1328

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135 Thr Thr Gly Arg Leu Gln Ser Gly Val Asn Thr Leu Gln Gly Phe Lys
136      375      380      385
138 gag gat aaa agg aac aaa gtc act cca gtg tta tat ttg aat tat ggg 1376
139 Glu Asp Lys Arg Asn Lys Val Thr Pro Val Leu Tyr Leu Asn Tyr Gly
140 390      395      400      405
142 ccc tac agt tct tat gca ccg cat tat gac tcc aca ttt gca aat atc 1424
143 Pro Tyr Ser Ser Tyr Ala Pro His Tyr Asp Ser Thr Phe Ala Asn Ile
144      410      415      420
146 agc aag gat gat tct gat tta atc tat tca acc tat ggg gaa gac tct 1472
147 Ser Lys Asp Asp Ser Asp Leu Ile Tyr Ser Thr Tyr Gly Glu Asp Ser
148      425      430      435
150 gat ctt cca agt gat ttc agc atc cat gag ttt ttg gcc acg tgc caa 1520
151 Asp Leu Pro Ser Asp Phe Ser Ile His Glu Phe Leu Ala Thr Cys Gln
152      440      445      450
154 gat tat ccg tat gtc atg gca gat agt tta ctg gat gtt tta aca aaa 1568
155 Asp Tyr Pro Tyr Val Met Ala Asp Ser Leu Leu Asp Val Leu Thr Lys
156      455      460      465
158 gga ggg cat tcc agg acc cta caa gag atg gag atg tca ttg cct gaa 1616
159 Gly Gly His Ser Arg Thr Leu Gln Glu Met Glu Met Ser Leu Pro Glu
160 470      475      480      485
162 gat gaa ggc cat act agg aca ctt gac aca gga aaa gaa atg gag cag 1664
163 Asp Glu Gly His Thr Arg Thr Leu Asp Thr Gly Lys Glu Met Glu Gln
164      490      495      500
166 att aca gaa gta gag cca cca ggg cgt ttg gac tcc agt act caa gac 1712
167 Ile Thr Glu Val Glu Pro Pro Gly Arg Leu Asp Ser Ser Thr Gln Asp
168      505      510      515
170 agg ctc ata gcg ctg aaa gca gta aca aat ttt ggc gtt cca gtt gaa 1760
171 Arg Leu Ile Ala Leu Lys Ala Val Thr Asn Phe Gly Val Pro Val Glu
172      520      525      530
174 gtt ttt gac tct gaa gaa gct gaa ata ttc cag aag aaa ctt gat gag 1808
175 Val Phe Asp Ser Glu Glu Ala Glu Ile Phe Gln Lys Lys Leu Asp Glu
176      535      540      545
178 acc acc aga ttg ctc agg gaa ctc cag gaa gcc cag aat gaa cgt ttg 1856
179 Thr Thr Arg Leu Leu Arg Glu Leu Gln Glu Ala Gln Asn Glu Arg Leu
180 550      555      560      565
182 agc acc aga ccc cct ggg aac atg atc tgt ctc ttg ggt ccc tca tca 1904
183 Ser Thr Arg Pro Pro Gly Asn Met Ile Cys Leu Leu Gly Pro Ser Ser
184      570      575      580
186 gag aaa tgc atc ttg ctg aac aag tgaccaataa tcttaagaa ttgcacagca 1958
187 Glu Lys Cys Ile Leu Leu Asn Lys
188      585
190 agtaactcca ggtgatatcg taagcacgta tggagttcga aaagcaatgg ggatttccat 2018
192 tccttcccc gtcattgaaa acaactttgt ggatttgaca gaagacactg aagaacctaa 2078
194 aaagacggat gttgatgagt gtcgacctgg tggaaagttga ggctgcctgg tatttgatta 2138
196 tatattatgt acatactttt tcattcttaa cttagaaatg cttttcagaa gatattaaat 2198
198 atttgtaaatt tgtgttttta attaaacttt tggaaacagc aatttggatg ttccagaggt 2258
200 tggacttgta ttaggtaata aagctggacc tgggactcgt gaggaagga 2307
203 <210> SEQ ID NO: 2
204 <211> LENGTH: 589

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206 <213> ORGANISM: PI3' Kinase
208 <400> SEQUENCE: 2
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210 1 5 10 15
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213 20 25 30
215 Glu Val Thr Glu Leu Ser Thr Gly Ser Ser Gly His Asp Ser Ser Leu
216 35 40 45
218 Phe Glu Asp Lys Asn Asp His Asp Lys His Lys Asp Arg Lys Arg Lys
219 50 55 60
221 Lys Arg Lys Lys Gly Glu Lys Gln Ile Pro Gly Glu Glu Lys Gly Arg
222 65 70 75 80
224 Lys Arg Arg Arg Val Lys Glu Asp Lys Lys Lys Arg Asp Arg Asp Arg
225 85 90 95
227 Val Glu Asn Glu Ala Glu Lys Asp Leu Gln Cys His Ala Pro Val Arg
228 100 105 110
230 Leu Asp Leu Pro Pro Glu Lys Pro Leu Thr Ser Ser Leu Ala Lys Gln
231 115 120 125
233 Glu Glu Val Glu Gln Thr Pro Leu Gln Glu Ala Leu Asn Gln Leu Met
234 130 135 140
236 Arg Gln Leu Gln Arg Lys Asp Pro Ser Ala Phe Phe Ser Phe Pro Val
237 145 150 155 160
239 Thr Asp Phe Ile Ala Pro Gly Tyr Ser Met Ile Ile Lys His Pro Met
240 165 170 175
242 Asp Phe Ser Thr Met Lys Glu Lys Ile Lys Asn Asn Asp Tyr Gln Ser
243 180 185 190
245 Ile Glu Glu Leu Lys Asp Asn Phe Lys Leu Met Cys Thr Asn Ala Met
246 195 200 205
248 Ile Tyr Asn Lys Pro Glu Thr Ile Tyr Tyr Lys Ala Ala Lys Lys Leu
249 210 215 220
251 Leu His Ser Gly Met Lys Ile Leu Ser Gln Glu Arg Ile Gln Ser Leu
252 225 230 235 240
254 Lys Gln Ser Ile Asp Phe Met Ala Asp Leu Gln Lys Thr Arg Lys Gln
255 245 250 255
257 Lys Asp Gly Thr Asp Thr Ser Gln Ser Gly Glu Asp Gly Gly Cys Trp
258 260 265 270
260 Gln Arg Glu Arg Glu Asp Ser Gly Asp Ala Glu Ala His Ala Phe Lys
261 275 280 285
263 Ser Pro Ser Lys Glu Asn Lys Lys Lys Asp Lys Asp Met Leu Glu Asp
264 290 295 300
266 Lys Phe Lys Ser Asn Asn Leu Glu Arg Glu Gln Glu Gln Leu Asp Arg
267 305 310 315 320
269 Ile Val Lys Glu Ser Gly Gly Lys Leu Thr Arg Arg Leu Val Asn Ser
270 325 330 335
272 Gln Cys Glu Phe Glu Arg Arg Lys Pro Asp Gly Thr Thr Thr Leu Gly
273 340 345 350
275 Leu Leu His Pro Val Asp Pro Ile Val Gly Glu Pro Gly Tyr Cys Leu
276 355 360 365

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278 Val Arg Leu Gly Met Thr Thr Gly Arg Leu Gln Ser Gly Val Asn Thr
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281 Leu Gln Gly Phe Lys Glu Asp Lys Arg Asn Lys Val Thr Pro Val Leu
282 385                      390                      395                      400
284 Tyr Leu Asn Tyr Gly Pro Tyr Ser Ser Tyr Ala Pro His Tyr Asp Ser
285                      405                      410                      415
287 Thr Phe Ala Asn Ile Ser Lys Asp Asp Ser Asp Leu Ile Tyr Ser Thr
288                      420                      425                      430
290 Tyr Gly Glu Asp Ser Asp Leu Pro Ser Asp Phe Ser Ile His Glu Phe
291                      435                      440                      445
293 Leu Ala Thr Cys Gln Asp Tyr Pro Tyr Val Met Ala Asp Ser Leu Leu
294                      450                      455                      460
296 Asp Val Leu Thr Lys Gly Gly His Ser Arg Thr Leu Gln Glu Met Glu
297 465                      470                      475                      480
299 Met Ser Leu Pro Glu Asp Glu Gly His Thr Arg Thr Leu Asp Thr Gly
300                      485                      490                      495
302 Lys Glu Met Glu Gln Ile Thr Glu Val Glu Pro Pro Gly Arg Leu Asp
303                      500                      505                      510
305 Ser Ser Thr Gln Asp Arg Leu Ile Ala Leu Lys Ala Val Thr Asn Phe
306                      515                      520                      525
308 Gly Val Pro Val Glu Val Phe Asp Ser Glu Glu Ala Glu Ile Phe Gln
309                      530                      535                      540
311 Lys Lys Leu Asp Glu Thr Thr Arg Leu Leu Arg Glu Leu Gln Glu Ala
312 545                      550                      555                      560
314 Gln Asn Glu Arg Leu Ser Thr Arg Pro Pro Gly Asn Met Ile Cys Leu
315                      565                      570                      575
317 Leu Gly Pro Ser Ser Glu Lys Cys Ile Leu Leu Asn Lys
318                      580                      585

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VERIFICATION SUMMARY                      DATE: 10/27/2000  
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Input Set : A:\1027-seq.app  
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L:39 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 1, CDS LOCATION:0..162